

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/525,180
Source: IFWP
Date Processed by STIC: 1/16/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/525,180

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/525,180

DATE: 01/16/2007
TIME: 15:08:55

Input Set : N:\SSLM\10525180.txt
Output Set: N:\CRF4\01162007\J525180.raw

*Use English in
a U.S. application*

W--> 1 SEQUENZPROTOKOLL SEQUENCE LISTING
3 <110> APPLICANT: Charite Universitatsmedizin Berlin
5 <120> TITLE OF INVENTION: Immunmarker zur Diagnostik and Therapie im Zusammenhang mit
6 Transplantat-Reaktionen
8 <130> FILE REFERENCE: P153902PC-La
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/525,180
C--> 11 <141> CURRENT FILING DATE: 2005-02-22
13 <150> PRIOR APPLICATION NUMBER: DE 102 38 922.5
14 <151> PRIOR FILING DATE: 2002-08-22
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: Patentln Ver. 2.1

*see item 4 on Euro
summary
sheet*

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES

65 <210> SEQ ID NO: 4
66 <211> LENGTH: 310
67 <212> TYPE: DNA
68 <213> ORGANISM: Rattus rattus
70 <400> SEQUENCE: 4
71 acattcatta ttaaagtga taatagaggt agaggtataa ataatatgaa ggggtgaggg 60
72 aaccagttct acccggttg tttggaatgc ttaaattatg taatttaaag agataatctt 120
E--> 73 tacttatgta ggtcttttgg aaata acttt ataaatttaa cacagaggac tactactaaa 180
E--> 74 cgtgagaggt atgataatcg gcatggaagt tgggtggtt gaccaccaa gttcaattct 240
E--> 75 taaagacatc ttaatcctga atataaaaat gcctttgtgg gtttagaatt agaattta 300
E--> 76 tttggcattt 310
122 <210> SEQ ID NO: 8
123 <211> LENGTH: 313
124 <212> TYPE: DNA
125 <213> ORGANISM: Rattus rattus
127 <400> SEQUENCE: 8
128 aggctagggc tagttctgcg gacctctcg gagagaggaa taaggttgaa ctgcctgtcc 60
129 ggttctcctt cccctattcc cagatgcagg tggagagcct cctctagtc tccccctaa 120
130 ccgcgacgaa gaccttggt aacacttgct cctttgcac accatagaaa atgcagtgc 180
131 gacaaacaca gctcgtcag gcgcttgagg agcgaagtc aatctgggtc ggcacctgca 240
132 ccaggctctt gcgcacctgg tcagaagacc ggcaccaat agttgcttat taaactctac 300
133 gtttgctccc aaa 313
E--> 134 ①

*invalid
nucleic
acid
designator*

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/525,180

DATE: 01/16/2007

TIME: 15:08:56

Input Set : N:\SSLM\10525180.txt

Output Set: N:\CRF4\01162007\J525180.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:73 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:181 SEQ:4
L:73 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=4
L:76 M:252 E: No. of Seq. differs, <211> LENGTH:Input:310 Found:311 SEQ:4
L:134 M:254 E: No. of Bases conflict, this line has no nucleotides.

10/525,180

3

SEQUENZPROTOKOLL

<110> Charite Universitätsmedizin Berlin

<120> Immunmarker zur Diagnostik and Therapie im Zusammenhang mit
Tranplantat-Reaktionen

<130> P153902PC-La

<140> PCT/EP03/09355

<141> 2003-08-22

change
to

<1507

<1517

these are prior application data